

Applicants: Yingru Wu, et al.
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Amendments to the Claims:

Please cancel claims 1-84 without disclaimer or prejudice to applicants' right to pursue the subject matters of these claims in the future.

Pursuant to 37 C.F.R. §1.121(c), this listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-84. (Cancelled)

85. (New) A method of altering fibre initiation and/or elongation in a fibre producing plant comprising manipulating said plant such that the production of a polypeptide is modified when compared to a wild-type plant, wherein the polypeptide is a transcription factor, regulatory protein, or a cell cycle protein, produced in said wild type plant at, or around, anthesis.

86. (New) The method of claim 85, wherein the polypeptide comprises a sequence selected from the group consisting of:

i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 16; or

ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 16.

87. (New) The method of claim 85 which comprises recombinantly expressing the polypeptide in said plant.

88. (New) The method of claim 85 which comprises reducing the level of the polypeptide endogenously produced by the plant.

89. (New) The method of claim 85, wherein the level of the polypeptide endogenously produced by the plant is reduced by exposing the plant to an antisense polynucleotide or a catalytic polynucleotide which hybridizes to an mRNA molecule encoding the polypeptide, and/or the level of the polypeptide endogenously produced by the plant is reduced by exposing the

plant to a dsRNA molecule that specifically down-regulates mRNA levels in a cell of an mRNA molecule encoding the polypeptide.

90. (New) The method of claim 85, wherein the plant is a species of the Genus *Gossypium*.

91. (New) A method of assessing the potential of a fibre producing plant to produce fibre, the method comprising analysing the plant for a genetic variation in a polynucleotide associated with fibre initiation and/or elongation, wherein the polynucleotide encodes a transcription factor, regulatory protein, or a cell cycle protein, produced in a wild type plant at, or around, anthesis, and/or the method comprising analysing the plant for a polypeptide involved in fibre initiation and/or elongation, wherein the polypeptide is a transcription factor, regulatory protein, or a cell cycle protein, produced in a wild type plant at, or around, anthesis.

92. (New) The method of claim 91, wherein the polynucleotide comprises a sequence selected from the group consisting of:

- i) a nucleotide sequence provided as any one of SEQ ID NO's:17 to 45; or
- ii) a nucleotide sequence which is at least 50% identical to any one of SEQ ID NO's:17 to 45.

93. (New) The method of claim 91, wherein the polypeptide comprises a sequence selected from the group consisting of:

- i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 16; or
- ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 16.

94. (New) A substantially purified and/or recombinant polypeptide selected from the group consisting of:

- i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:1,

ii) a polypeptide comprising an amino acid sequence which is at least 87% identical to SEQ ID NO:1,

iii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:2,

iv) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:3,

v) a polypeptide comprising an amino acid sequence which is at least 54% identical to SEQ ID NO:3,

vi) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:4,

vii) a polypeptide comprising an amino acid sequence which is at least 55% identical to SEQ ID NO:4,

viii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:5,

ix) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:5,

x) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:6,

xi) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:6,

xii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:7,

xiii) a polypeptide comprising an amino acid sequence which is at least 79% identical to SEQ ID NO:7,

xiv) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:8,

xv) a polypeptide comprising an amino acid sequence which is at least 66% identical to SEQ ID NO:8,

xvi) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:9,

xvii) a polypeptide comprising an amino acid sequence which is at least 95% identical to SEQ ID NO:9,

xviii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:10,

xix) a polypeptide comprising an amino acid sequence which is at least 67% identical to SEQ ID NO:10,

xx) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:11,

xxi) a polypeptide comprising an amino acid sequence which is at least 55% identical to SEQ ID NO:11,

xxii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:12,

xxiii) a polypeptide comprising an amino acid sequence which is at least 59% identical to SEQ ID NO:12,

xxiv) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:13,

xxv) a polypeptide comprising an amino acid sequence which is at least 77% identical to SEQ ID NO:13,

xxvi) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:14,

xxvii) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:14,

xxviii) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:15,

xxix) a polypeptide comprising an amino acid sequence which is at least 64% identical to SEQ ID NO:15,

xxx) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:16,

xxxi) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:16, and

xxxii) a biologically active fragment of i) or xxxi), wherein the polypeptide regulates fibre initiation and/or elongation.

95. (New) An isolated and/or exogenous polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

i) a sequence of nucleotides as provided in SEQ ID NO:17;

ii) a sequence of nucleotides as provided in SEQ ID NO:18;

iii) a sequence of nucleotides which is at least 87% identical to SEQ ID NO:17 or SEQ ID NO:18;

iv) a sequence of nucleotides as provided in SEQ ID NO:19;

v) a sequence of nucleotides as provided in SEQ ID NO:20;

vi) a sequence complementary to iv) or v);

- vii) a sequence of nucleotides as provided in SEQ ID NO:21;
- viii) a sequence of nucleotides as provided in SEQ ID NO:22;
- ix) a sequence of nucleotides which is at least 54% identical to SEQ ID NO:21 or SEQ ID NO:22;
- x) a sequence of nucleotides as provided in SEQ ID NO:23;
- xi) a sequence of nucleotides which is at least 55% identical to SEQ ID NO:23;
- xii) a sequence of nucleotides as provided in SEQ ID NO:24;
- xiii) a sequence of nucleotides as provided in SEQ ID NO:25;
- xiv) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:24 or SEQ ID NO:25;
- xv) a sequence of nucleotides as provided in SEQ ID NO:26;
- xvi) a sequence of nucleotides as provided in SEQ ID NO:27;
- xvii) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:26 or SEQ ID NO:27;
- xviii) a sequence of nucleotides as provided in SEQ ID NO:28;
- xix) a sequence of nucleotides as provided in SEQ ID NO:29;
- xx) a sequence complementary to xviii) or xix);
- xxi) a sequence of nucleotides as provided in SEQ ID NO:30;
- xxii) a sequence of nucleotides as provided in SEQ ID NO:31;
- xxiii) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:30 or SEQ ID NO:31;
- xxiv) a sequence of nucleotides as provided in SEQ ID NO:32,
- xxv) a sequence of nucleotides as provided in SEQ ID NO:33,
- xxvi) a sequence complementary to xxiv) or xxv),
- xxvii) a sequence of nucleotides as provided in SEQ ID NO:34;

xxviii) a sequence of nucleotides as provided in SEQ ID NO:35;

xxix) a sequence of nucleotides which is at least 70% identical to SEQ ID NO:34 or SEQ ID NO:35;

xxx) a sequence of nucleotides as provided in SEQ ID NO:36;

xxxi) a sequence of nucleotides as provided in SEQ ID NO:37;

xxxii) a sequence of nucleotides which is at least 55% identical to SEQ ID NO:36 or SEQ ID NO:37;

xxxiii) a sequence of nucleotides as provided in SEQ ID NO:38;

xxxiv) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:38;

xxxv) a sequence of nucleotides as provided in SEQ ID NO:39;

xxxvi) a sequence of nucleotides as provided in SEQ ID NO:40;

xxxvii) a sequence of nucleotides which is at least 95% identical to SEQ ID NO:39 or SEQ ID NO:40;

xxxviii) a sequence of nucleotides as provided in SEQ ID NO:41;

xxxix) a sequence of nucleotides as provided in SEQ ID NO:42;

xl) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:41 or SEQ ID NO:42;

xli) a sequence of nucleotides as provided in SEQ ID NO:43;

xlii) a sequence of nucleotides as provided in SEQ ID NO:44;

xliii) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:43 or SEQ ID NO:44;

xliv) a sequence of nucleotides as provided in SEQ ID NO:45;

xlv) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:45;

xlvi) a sequence encoding a polypeptide according to claim 94;

xlvi) a sequence which hybridizes to any one of i) to iii), vii) to xvii), xxi) to xxiii) or xxvii) to xlvi) under high stringency conditions; and

xlvi) a sequence which is at least 19 contiguous nucleotides of a polynucleotide according to any one of i) to xlii),

wherein the polynucleotide does not comprise a sequence of nucleotides as provided in any one of SEQ ID NO's 46 to 57.

96. (New) A polynucleotide which is:

i) catalytic polynucleotide capable of cleaving a polynucleotide of claim 95, or

ii) a double stranded RNA (dsRNA) molecule comprising an polynucleotide according to part xlviii) of claim 95, wherein the portion of the molecule that is double stranded is at least 19 basepairs in length and comprises said polynucleotide.

97. (New) A vector comprising or encoding the polynucleotide of claim 95.

98. (New) A vector comprising or encoding the polynucleotide of claim 96.

99. (New) A host cell comprising the vector of claim 97.

100. (New) A host cell comprising the vector of claim 98.

101. (New) A transgenic plant, the plant having been transformed with the polynucleotide of claim 95.

102. (New) A transgenic plant, the plant having been transformed such that it produces the polynucleotide of claim 96.

103. (New) A method of breeding a fibre producing plant, the method comprising performing a method of claim 91.

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104. (New) A method of selecting from a breeding population a fibre producing plant with altered fibre initiation and/or elongation potential, the method comprising;

i) crossing two plants which have differing potential to produce fibre,

ii) performing a method of claim 91 on progeny plants,

iii) selecting a progeny plant with altered fibre initiation and/or elongation potential when compared to a parent plant.

105. (New) A plant produced by the method of claim 103.

106. (New) A plant produced by the method of claim 104.

107. (New) Transgenic seed of a plant of claim 101.

108. (New) Transgenic seed of a plant of claim 102.

109. (New) Transgenic fibre of a plant of claim 101.

110. (New) Transgenic fibre of a plant of claim 102.

111. (New) A method of identifying an agent which alters fibre initiation and/or elongation of a fibre producing plant, the method comprising

a) exposing a polynucleotide which is at least 50% identical to any one of SEQ ID NO's:17 to 45 to a candidate agent, and

b) assessing the ability of the candidate agent to hybridize and/or cleave the polynucleotide.

112. (New) A transgenic fibre producing plant which, when compared to an isogenic non-transgenic plant, produces a modified level of a polypeptide which is a transcription factor, regulatory protein, or a cell cycle protein, wherein the polypeptide is produced in said non-transgenic plant at, or around, anthesis.

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113. (New) A transgenic fibre producing plant which, when compared to an isogenic non-transgenic plant, produces a modified level of a polypeptide which is a transcription factor, regulatory protein, or a cell cycle protein, wherein the polypeptide is produced in said non-transgenic plant at, or around, anthesis, wherein the polypeptide comprises a sequence selected from the group consisting of:

i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 16; or

ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 16.

114. (New) A transgenic fibre producing plant which, when compared to an isogenic non-transgenic plant, produces a modified level of a polypeptide which is a transcription factor, regulatory protein, or a cell cycle protein, wherein the polypeptide is produced in said non-transgenic plant at, or around, anthesis, wherein the plant comprises a polynucleotide of claim 96.

115. (New) Transgenic seed of a plant of claim 112.

116. (New) Transgenic fibre of a plant of claim 112.